



#7

SEQUENCE LISTING

<110> Cases, Sylvaine
Stone, Scot
Zhou, Ping
Farese, Robert V.
Chi-Liang Eric Yen

<120> DIACYLGLYCEROL O-ACYLTRANSFERASE 2a
(DGAT2a)

<130> UCAL240CIP

<140> US 10/046,924

<141> 2002-01-14

<150> 60/271,307

<151> 2001-02-23

<150> 09/794,715

<151> 2001-02-26

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1231

<212> DNA

<213> Homo sapiens

<400> 1

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cttccttgta	ctgggagtgg	cctgcagtgc	catcctcatg	tacatattct	gcactgattg	300
ctggctcatc	gctgtgctct	acttcacttg	gctgggtgtt	gactggaaca	cacccaagaa	360
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caccatagac	tatttgcttt	caaagaatgg	gagtggaat	gctatcatca	tcgtggctcg	720
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tggagagaat	gaagtgtaca	agcaggtgat	cttcgaggag	ggctcctggg	gccgatgggt	900
ccagaagaag	ttccagaaat	acattgggtt	cgccccatgc	atcttccatg	gtcgaggcct	960
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caccatgtac	atggaggccc	tgggtgaagct	cttcgacaag	cacaagacca	agttcggcct	1140
cccggagact	gagggtcctg	aggtgaactg	agccagcctt	cggggccaat	tccttgagg	1200
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<210> 2

<211> 388
 <212> PRT
 <213> Homo sapiens

<400> 2

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			20					25					30		
Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	Ile	Leu	Ser
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Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	Arg	Ser	Lys	Val
	50					55					60				
Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	Trp	Val	Leu	Ser	Phe
65					70					75					80
Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	Leu	Met	Tyr	Ile	Phe	Cys
				85					90					95	
Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	Tyr	Phe	Thr	Trp	Leu	Val	Phe
			100						105					110	
Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg
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Asn	Trp	Ala	Val	Trp	Arg	Tyr	Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu
	130					135					140				
Val	Lys	Thr	His	Asn	Leu	Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr
145					150					155					160
His	Pro	His	Gly	Ile	Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr
				165					170					175	
Glu	Ala	Thr	Glu	Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu
			180					185					190		
Ala	Thr	Leu	Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu
	195						200					205			
Met	Ser	Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu
	210					215					220				
Leu	Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
225					230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	Leu
				245					250					255	
Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly	Ala	Asp
			260					265					270		
Leu	Val	Pro	Ile	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr	Lys	Gln	Val
		275					280					285			
Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Gln	Lys	Lys	Phe	Gln
	290					295					300				
Lys	Tyr	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His	Gly	Arg	Gly	Leu	Phe
305					310					315					320
Ser	Ser	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr	Ser	Lys	Pro	Ile	Thr	Thr
			325						330					335	
Val	Val	Gly	Glu	Pro	Ile	Thr	Ile	Pro	Lys	Leu	Glu	His	Pro	Thr	Gln
			340					345					350		
Gln	Asp	Ile	Asp	Leu	Tyr	His	Thr	Met	Tyr	Met	Glu	Ala	Leu	Val	Lys
		355					360					365			
Leu	Phe	Asp	Lys	His	Lys	Thr	Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val
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Leu	Glu	Val	Asn												
385															

<210> 3

<211> 1167
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)...(1167)
 <223> n = A,T,C or G

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ggcactggct ccagcatcct ctcagccctc caagacatct tctctgtcac ctggctcaac    180
agatcyaagg tggaaaaaca gctgcaggtc atctcagtac tacaatgggt cctatccttc    240
ctgggtgctag gagtggcctg cagtgtcatc ctcatgtaca ccttctgcac agactgctgg    300
ctgatagctg tgctctactt cacctggctg gcatttgact ggaacacgcc caagaaaggt    360
ggcaggagat cgcagtgggt gcgaaactgg gccgtgtggc gctacttccg agactacttt    420
cccatccagc tgggtgaagac acacaacctg ctgaccacca ggaactatat ctttggatac    480
caccatcatg gcatcatggg cctgggtgcc ttctgtaact tcagcacaga ggctactgaa    540
gtcagcaaga agtttcctgg cataaggccc tatttggcta cgttggcygg taacttccgg    600
atgcctgtgc ttccgcgagta cctgatgtct ggaggcatct gccctgtcaa ccgagacacc    660
atagactact tgctctccaa gaatgggagt ggcaatgcta tcatcatcgt ggtgggaggt    720
gcagctgagt ccctgagctc catgcctggc aagaacgcag tcaccctgaa gaaccgaaa    780
ggctttgtga agctggccct gcgccatgga gctgatctgg ttcccactta ttcctttgga    840
gagaatgagg tatacaagca ggtgatcttt gaggagggtt cctggggccg atgggtccag    900
aagaagttcc agaagtatat tggtttcgcc ccctgcatct tccatggccg aggcctcttc    960
tcctctgaca cctggggggt ggtgccctac tccaagccca tcaccaccgt cgtgggggag   1020
cccatcactg tccccaaagt ggagcaccgc acccagaaag acatcgacct gtaccatgcc   1080
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<210> 4
 <211> 387
 <212> PRT
 <213> Mus musculus

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 20             25             30
Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser
 35             40             45
Ala Leu Gln Asp Ile Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val
 50             55             60
Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe
 65             70             75             80
Leu Val Leu Gly Val Ala Cys Ser Val Ile Leu Met Tyr Thr Phe Cys
 85             90             95
Thr Asp Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Ala Phe
100             105             110
Asp Trp Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg
115             120             125
Asn Trp Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu
130             135             140
Val Lys Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr
145             150             155             160
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<212> PRT
 <213> Mus musculus

<400> 6

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		20					25						30		
Gln	Val	Cys	Ile	Gly	Ile	Met	Val	Met	Leu	Val	Leu	Tyr	Asn	Tyr	Trp
	35					40						45			
Phe	Leu	Tyr	Ile	Pro	Tyr	Leu	Val	Trp	Phe	Tyr	Tyr	Asp	Trp	Arg	Thr
50						55					60				
Pro	Glu	Gln	Gly	Gly	Arg	Arg	Trp	Asn	Trp	Val	Gln	Ser	Trp	Pro	Val
65					70					75					80
Trp	Lys	Tyr	Phe	Lys	Glu	Tyr	Phe	Pro	Ile	Cys	Leu	Val	Lys	Thr	Gln
				85					90					95	
Asp	Leu	Asp	Pro	Gly	His	Asn	Tyr	Ile	Phe	Gly	Phe	His	Pro	His	Gly
			100					105					110		
Ile	Phe	Val	Pro	Gly	Ala	Phe	Gly	Asn	Phe	Cys	Thr	Lys	Tyr	Ser	Asp
	115						120					125			
Phe	Lys	Lys	Leu	Phe	Pro	Gly	Phe	Thr	Ser	Tyr	Leu	His	Val	Ala	Lys
	130					135					140				
Ile	Trp	Phe	Cys	Phe	Pro	Leu	Phe	Arg	Glu	Tyr	Leu	Met	Ser	Asn	Gly
145					150					155					160
Pro	Val	Ser	Val	Ser	Lys	Glu	Ser	Leu	Ser	His	Val	Leu	Ser	Lys	Asp
				165					170					175	
Gly	Gly	Gly	Asn	Val	Ser	Ile	Ile	Val	Leu	Gly	Gly	Ala	Lys	Glu	Ala
			180					185					190		
Leu	Glu	Ala	His	Pro	Gly	Thr	Phe	Thr	Leu	Cys	Ile	Arg	Gln	Arg	Lys
	195						200					205			
Gly	Phe	Val	Lys	Met	Ala	Leu	Thr	His	Gly	Ala	Ser	Leu	Val	Pro	Val
	210					215					220				
Phe	Ser	Phe	Gly	Glu	Asn	Asp	Leu	Tyr	Lys	Gln	Ile	Asn	Asn	Pro	Lys
225					230					235					240
Gly	Ser	Trp	Leu	Arg	Thr	Ile	Gln	Asp	Ala	Met	Tyr	Asp	Ser	Met	Gly
				245					250					255	
Val	Ala	Leu	Pro	Leu	Ile	Tyr	Ala	Arg	Gly	Ile	Phe	Gln	His	Tyr	Phe
			260					265					270		
Gly	Ile	Met	Pro	Tyr	Arg	Lys	Leu	Ile	Tyr	Thr	Val	Val	Gly	Arg	Pro
	275					280						285			
Ile	Pro	Val	Gln	Gln	Ile	Leu	Asn	Pro	Thr	Ser	Glu	Gln	Ile	Glu	Glu
	290					295					300				
Leu	His	Gln	Thr	Tyr	Leu	Glu	Glu	Leu	Lys	Lys	Leu	Phe	Asn	Glu	His
305					310					315					320
Lys	Gly	Lys	Tyr	Gly	Ile	Pro	Glu	His	Glu	Thr	Leu	Val	Phe	Lys	
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<210> 7
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<400> 7

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gtcctttctt	ttcttacagg	gccgatgtcc	attggaatca	ctgtgatgct	gatcatacac	180
aactatttgt	tcctttacat	cccttatttg	atgtggcttt	actttgactg	gcatacccca	240

gagcggaggag	gcaggagatc	cagctggatc	aaaaattgga	ctctttggaa	acactttaag	300
gactatttttc	caattcatct	tatcaaaact	caagatttgg	atccaagtca	caactatata	360
tttgggtttc	accccatgg	aataatggca	gttggagcct	ttgggaattt	ttctgtaaat	420
tattctgact	tcaaggacct	gtttcctggc	tttacttcat	atcttcacgt	gctgccactt	480
tggttctggg	gtcctgtctt	tcgagaatat	gtgatgagtg	ttgggctggg	ttcagtttcc	540
aagaaaagtg	tgtcctacat	ggtaagcaag	gagggagggtg	gaaacatctc	tgtcattgtc	600
cttgggggtg	caaaaagaatc	actggatgct	catcctggaa	agttcactct	gttcacccgc	660
cagcggaaaag	gatttggttaa	aattgctttg	acccatggcg	cctctctggg	cccagtggtt	720
tcttttggtg	aaaatgaact	gtttaaacaa	actgacaacc	ctgaaggatc	atggattaga	780
actgttcaga	ataaactgca	gaagatcatg	gggtttgctt	tgcccctgtt	tcatgccagg	840
ggagtttttc	agtacaattt	tggcctaattg	acctatagga	aagccatcca	cactgttggt	900
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catcagacct	atatggagga	acttaggaaa	ttgtttgagg	aacacaaaagg	aaagtatggc	1020
attccagagc	acgagactct	tgttttaaaa	tgacttgact	ataaaaaaaaa	attaaaaaat	1080
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<210> 8

<211> 334

<212> PRT

<213> Homo sapiens

<400> 8

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Gln	Thr	Val	Ala	Val	Leu	Gln	Trp	Val	Leu	Ser	Phe	Leu	Thr	Gly	Pro
		20					25				30				
Met	Ser	Ile	Gly	Ile	Thr	Val	Met	Leu	Ile	Ile	His	Asn	Tyr	Leu	Phe
	35					40					45				
Leu	Tyr	Ile	Pro	Tyr	Leu	Met	Trp	Leu	Tyr	Phe	Asp	Trp	His	Thr	Pro
	50				55					60					
Glu	Arg	Gly	Gly	Arg	Arg	Ser	Ser	Trp	Ile	Lys	Asn	Trp	Thr	Leu	Trp
65				70					75					80	
Lys	His	Phe	Lys	Asp	Tyr	Phe	Pro	Ile	His	Leu	Ile	Lys	Thr	Gln	Asp
			85					90						95	
Leu	Asp	Pro	Ser	His	Asn	Tyr	Ile	Phe	Gly	Phe	His	Pro	His	Gly	Ile
	100						105				110				
Met	Ala	Val	Gly	Ala	Phe	Gly	Asn	Phe	Ser	Val	Asn	Tyr	Ser	Asp	Phe
	115					120					125				
Lys	Asp	Leu	Phe	Pro	Gly	Phe	Thr	Ser	Tyr	Leu	His	Val	Leu	Pro	Leu
	130				135					140					
Trp	Phe	Trp	Cys	Pro	Val	Phe	Arg	Glu	Tyr	Val	Met	Ser	Val	Gly	Leu
145				150					155					160	
Val	Ser	Val	Ser	Lys	Lys	Ser	Val	Ser	Tyr	Met	Val	Ser	Lys	Glu	Gly
		165						170						175	
Gly	Gly	Asn	Ile	Ser	Val	Ile	Val	Leu	Gly	Gly	Ala	Lys	Glu	Ser	Leu
	180						185					190			
Asp	Ala	His	Pro	Gly	Lys	Phe	Thr	Leu	Phe	Ile	Arg	Gln	Arg	Lys	Gly
	195					200					205				
Phe	Val	Lys	Ile	Ala	Leu	Thr	His	Gly	Ala	Ser	Leu	Val	Pro	Val	Val
	210				215					220					
Ser	Phe	Gly	Glu	Asn	Glu	Leu	Phe	Lys	Gln	Thr	Asp	Asn	Pro	Glu	Gly
225				230					235					240	
Ser	Trp	Ile	Arg	Thr	Val	Gln	Asn	Lys	Leu	Gln	Lys	Ile	Met	Gly	Phe
		245					250						255		
Ala	Leu	Pro	Leu	Phe	His	Ala	Arg	Gly	Val	Phe	Gln	Tyr	Asn	Phe	Gly
	260					265					270				
Leu	Met	Thr	Tyr	Arg	Lys	Ala	Ile	His	Thr	Val	Val	Gly	Arg	Pro	Ile


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<210> 14
<211> 333
<212> PRT
<213> Homo sapiens

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<400> 14
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 20          25          30
Ile Ala Val Asn Leu Tyr Leu Val Val Phe Thr Pro Tyr Trp Pro Val
 35          40          45
Thr Val Leu Ile Leu Thr Trp Leu Ala Phe Asp Trp Lys Thr Pro Gln
 50          55          60
Arg Gly Gly Arg Arg Phe Thr Cys Val Arg His Trp Arg Leu Trp Lys
 65          70          75          80
His Tyr Ser Asp Tyr Phe Pro Leu Lys Leu Leu Lys Thr His Asp Ile
 85          90          95
Cys Pro Ser Arg Asn Tyr Ile Leu Val Cys His Pro His Gly Leu Phe
100          105          110
Ala His Gly Trp Phe Gly His Phe Ala Thr Glu Ala Ser Gly Phe Ser
115          120          125
Lys Ile Phe Pro Gly Ile Thr Pro Tyr Ile Leu Thr Leu Gly Ala Phe
130          135          140
Phe Trp Met Pro Phe Leu Arg Glu Tyr Val Met Ser Thr Gly Ala Cys
145          150          155          160
Ser Val Ser Arg Ser Ser Ile Asp Phe Leu Leu Thr His Lys Gly Thr
165          170          175
Gly Asn Met Val Ile Val Val Ile Gly Gly Leu Ala Glu Cys Arg Tyr
180          185          190
Ser Leu Pro Gly Ser Ser Thr Leu Val Leu Lys Asn Arg Ser Gly Phe
195          200          205
Val Arg Met Ala Leu Gln His Gly Val Pro Leu Ile Pro Ala Tyr Ala
210          215          220
Phe Gly Glu Thr Asp Leu Tyr Asp Gln His Ile Phe Thr Pro Gly Gly
225          230          235          240
Phe Val Asn Arg Phe Gln Lys Trp Phe Gln Ser Met Val His Ile Tyr
245          250          255
Pro Cys Ala Phe Tyr Gly Arg Gly Phe Thr Lys Asn Ser Trp Gly Leu
260          265          270
Leu Pro Tyr Ser Arg Pro Val Thr Thr Ile Val Gly Glu Pro Leu Pro
275          280          285
Met Pro Lys Ile Glu Asn Pro Ser Gln Glu Ile Val Ala Lys Tyr His
290          295          300
Thr Leu Tyr Ile Asp Ala Leu Arg Lys Leu Phe Asp Gln His Lys Thr
305          310          315          320
Lys Phe Gly Ile Ser Glu Thr Gln Glu Leu Glu Ile Ile

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<210> 15
 <211> 1050
 <212> DNA
 <213> Homo sapiens

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 ttctccttct tggcactggg taagatctgc actgtgggct tcatagccct cctgtttaca 180
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 gactatttcc ccatccagct ggtcaagact gctgagctgg acccctctcg gaactacatt 360
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 aaccgaaagg gcttcgtcag gctgcacctg acacacgggg cacccttggt gccaatcttc 720
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 ggtgtcttcc agtacagctt tggtttaata ccctaccgcc ggcccatcac cactgtgggg 900
 aagcccatcg aggtacagaa gacgtgcat ccctcggagg aggaggtgaa ccagctgcac 960
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 cctgtgacc agcacttgga gttctgctga 1050

<210> 16
 <211> 333
 <212> PRT
 <213> Homo sapiens

<400> 16
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 Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu
 35 40 45
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